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TECH CENTER 1600/2900

## SEQUENCE LISTING

<110> Selden, Richard F.  
Miller, Allan M.  
Treco, Douglas A.

<120> OPTIMIZED MESSENGER RNA

<130> 10278-022001

<140> 09/686,497

<141> 2000-10-11

<150> 09/407,605

<151> 1999-09-28

<150> 60/130,241

<151> 1999-04-20

<150> 60/102,239

<151> 1998-09-29

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<212> DNA

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Cys	Leu	Leu	Arg	Phe	Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	
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gcc	gtg	gag	ctg	agc	tgg	gac	tac	atg	cag	agc	gac	ctg	ggc	gag	ctg	147
Ala	Val	Glu	Leu	Ser	Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	
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Pro	Val	Asp	Ala	Arg	Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	
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aac	acc	agc	gtg	gtg	tac	aag	aag	acc	ctg	ttc	gtg	gag	ttc	acc	gac	243
Asn	Thr	Ser	Val	Val	Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	

60	65	70	75	
cac ctg ttc aac atc gcc aag ccc cgc ccc ccc tgg atg ggc ctg ctg				291
His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu	80	85	90	
ggc ccc acc atc cag gcc gag gtg tac gac acc gtg gtg atc acc ctg				339
Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu	95	100	105	
aag aac atg gcc agc cac ccc gtg agc ctg cac gcc gtg ggc gtg agc				387
Lys Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val Ser	110	115	120	
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Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln	125	130	135	
cgc gag aag gag gac gac aag gtg ttc ccc ggc ggc agc cac acc tac				483
Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr	140	145	150	155
gtg tgg cag gtg ctg aag gag aac ggc ccc atg gcc agc gac ccc ctg				531
Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu	160	165	170	
tgc ctg acc tac agc tac ctg agc cac gtg gac ctg gtg aag gac ctg				579
Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu	175	180	185	
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Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu	190	195	200	
gcc aag gag aag acc cag acc ctg cac aag ttc atc ctg ctg ttc gcc				675
Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala	205	210	215	
gtg ttc gac gag ggc aag agc tgg cac agc gag acc aag aac agc ctg				723
Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu	220	225	230	235
atg cag gac cgc gac gcc gcc agc gcc cgc gcc tgg ccc aag atg cac				771
Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His	240	245	250	
acc gtg aac ggc tac gtg aac cgc agc ctg ccc ggc ctg atc ggc tgc				819
Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys	255	260	265	
cac cgc aag agc gtg tac tgg cac gtg atc ggc atg ggc acc acc ccc				867
His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro	270	275	280	
gag gtg cac agc atc ttc ctg gag ggc cac acc ttc ctg gtg cgc aac				915
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn	285	290	295	

cac cgc cag gcc agc ctg gag atc agc ccc atc acc ttc ctg acc gcc His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala 300 305 310 315	963
cag acc ctg ctg atg gac ctg ggc cag ttc ctg ctg ttc tgc cac atc Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile 320 325 330	1011
agc agc cac cag cac gac ggc atg gag gcc tac gtg aag gtg gac agc Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser 335 340 345	1059
tgc ccc gag gag ccc cag ctg cgc atg aag aac aac gag gag gcc gag Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu 350 355 360	1107
gac tac gac gac gac ctg acc gac agc gag atg gac gtg gtg cgc ttc Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe 365 370 375	1155
gac gac gac aac agc ccc agc ttc atc cag atc cgc agc gtg gcc aag Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys 380 385 390 395	1203
aag cac ccc aag acc tgg gtg cac tac atc gcc gcc gag gag gag gac Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp 400 405 410	1251
tgg gac tac gcc ccc ctg gtg ctg gcc ccc gac gac cgc agc tac aag Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys 415 420 425	1299
agc cag tac ctg aac aac ggc ccc cag cgc atc ggc cgc aag tac aag Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys 430 435 440	1347
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gtg ggc gac acc ctg ctg atc atc ttc aag aac cag gcc agc cgc ccc Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro 480 485 490	1491
tac aac atc tac ccc cac ggc atc acc gac gtg cgc ccc ctg tac agc Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser 495 500 505	1539
cgc cgc ctg ccc aag ggc gtg aag cac ctg aag gac ttc ccc atc ctg Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu 510 515 520	1587

ccc ggc gag atc ttc aag tac aag tgg acc gtg acc gtg gag gac ggc Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly 525 530 535	1635
ccc acc aag agc gac ccc cgc tgc ctg acc cgc tac tac agc agc ttc Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe 540 545 550 555	1683
gtg aac atg gag cgc gac ctg gcc agc ggc ctg atc ggc ccc ctg ctg Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu 560 565 570	1731
atc tgc tac aag gag agc gtg gac cag cgc ggc aac cag atc atg agc Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser 575 580 585	1779
gac aag cgc aac gtg atc ctg ttc agc gtg ttc gac gag aac cgc agc Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser 590 595 600	1827
tgg tac ctg acc gag aac atc cag cgc ttc ctg ccc aac ccc gcc ggc Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly 605 610 615	1875
gtg cag ctg gag gac ccc gag ttc cag gcc agc aac atc atg cac agc Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser 620 625 630 635	1923
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gag gtg gcc tac tgg tac atc ctg agc atc ggc gcc cag acc gac ttc Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe 655 660 665	2019
ctg agc gtg ttc ttc agc ggc tac acc ttc aag cac aag atg gtg tac Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr 670 675 680	2067
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agc atg gag aac ccc ggc ctg tgg atc ctg ggc tgc cac aac agc gac Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp 700 705 710 715	2163
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aag aac acc ggc gac tac tac gag gac agc tac gag gac atc agc gcc Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala 735 740 745	2259
tac ctg ctg agc aag aac aac gcc atc gag ccc cgc ctg gag gag atc	2307

Tyr	Leu	Leu	Ser	Lys	Asn	Asn	Ala	Ile	Glu	Pro	Arg	Leu	Glu	Glu	Ile	
	750						755					760				
acc	cgc	acc	acc	ctg	cag	agc	gac	cag	gag	gag	atc	gac	tac	gac	gac	2355
Thr	Arg	Thr	Thr	Leu	Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	
	765					770					775					
acc	atc	agc	gtg	gag	atg	aag	aag	gag	gac	ttc	gac	atc	tac	gac	gag	2403
Thr	Ile	Ser	Val	Glu	Met	Lys	Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	
	780				785				790						795	
gac	gag	aac	cag	agc	ccc	cgc	agc	ttc	cag	aag	aag	acc	cgc	cac	tac	2451
Asp	Glu	Asn	Gln	Ser	Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	
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ttc	atc	gcc	gcc	gtg	gag	cgc	ctg	tgg	gac	tac	ggc	atg	agc	agc	agc	2499
Phe	Ile	Ala	Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	
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ccc	cac	gtg	ctg	cgc	aac	cgc	gcc	cag	agc	ggc	agc	gtg	ccc	cag	ttc	2547
Pro	His	Val	Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	
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aag	aag	gtg	gtg	ttc	cag	gag	ttc	acc	gac	ggc	agc	ttc	acc	cag	ccc	2595
Lys	Lys	Val	Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	
	845					850					855					
ctg	tac	cgc	ggc	gag	ctg	aac	gag	cac	ctg	ggc	ctg	ctg	ggc	ccc	tac	2643
Leu	Tyr	Arg	Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	
	860				865				870						875	
atc	cgc	gcc	gag	gtg	gag	gac	aac	atc	atg	gtg	acc	ttc	cgc	aac	cag	2691
Ile	Arg	Ala	Glu	Val	Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	
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gcc	agc	cgc	ccc	tac	agc	ttc	tac	agc	agc	ctg	atc	agc	tac	gag	gag	2739
Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	
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gac	cag	cgc	cag	ggc	gcc	gag	ccc	cgc	aag	aac	ttc	gtg	aag	ccc	aac	2787
Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	Pro	Asn	
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Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	
	925					930					935					
aag	gac	gag	ttc	gac	tgc	aag	gcc	tgg	gcc	tac	ttc	agc	gac	gtg	gac	2883
Lys	Asp	Glu	Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	
	940				945					950					955	
ctg	gag	aag	gac	gtg	cac	agc	ggc	ctg	atc	ggg	ccc	ctg	ctg	gtg	tgc	2931
Leu	Glu	Lys	Asp	Val	His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	
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cac	acc	aac	acc	ctg	aac	ccc	gcc	cac	ggc	cgc	cag	gtg	acc	gtg	cag	2979
His	Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	

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990	995	1000	
ttc acc gag aac atg gag cgc aac tgc cgc gcc ccc tgc aac atc cag			3075
Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln			
1005	1010	1015	
atg gag gac ccc acc ttc aag gag aac tac cgc ttc cac gcc atc aac			3123
Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn			
1020	1025	1030	1035
ggc tac atc atg gag acc ctg aaa ggc ctg gtg atg gcc cag gac cag			3171
Gly Tyr Ile Met Asp Thr Leu Lys Gly Leu Val Met Ala Gln Asp Gln			
	1040	1045	1050
cgc atc cgc tgg tac ctg ctg agc atg ggc agc aac gag aac atc cac			3219
Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His			
	1055	1060	1065
agc atc cac ttc agc ggc cac gtg ttc acc gtg cgc aag aag gag gag			3267
Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu			
	1070	1075	1080
tac aag atg gcc ctg tac aac ctg tac ccc ggc gtg ttc gag acc gtg			3315
Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val			
	1085	1090	1095
gag atg ctg ccc agc aag gcc ggc atc tgg cgc gtg gag tgc ctg atc			3363
Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile			
1100	1105	1110	1115
ggc gag cac ctg cac gcc ggc atg agc acc ctg ttc ctg gtg tac agc			3411
Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser			
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aac aag tgc cag acc ccc ctg ggc atg gcc agc ggc cac atc cgc gac			3459
Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp			
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ttc cag atc acc gcc agc ggc cag tac ggc cag tgg gcc ccc aag ctg			3507
Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu			
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gcc cgc ctg cac tac agc ggc agc atc aac gcc tgg agc acc aag gag			3555
Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu			
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ccc ttc agc tgg atc aag gtg gac ctg ctg gcc ccc atg atc atc cac			3603
Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His			
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ggc atc aag acc cag ggc gcc cgc cag aac ttc agc agc ctg tac atc			3651
Gly Ile Lys Thr Gln Gly Ala Arg Gln Asn Phe Ser Ser Leu Tyr Ile			
	1200	1205	1210

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  Cys Leu Leu Arg Phe Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly  
                   15                  20                  25

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  Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu  
                   30                  35                  40

ccc gtg gac gcc cgc ttc ccc ccc cgc gtg ccc aag agc ttc ccc ttc 195  
  Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe  
                   45                  50                  55

aac acc agc gtg gtg tac aag aag acc ctg ttc gtg gag ttc acc gac 243  
  Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp  
                   60                  65                  70                  75

cac ctg ttc aac atc gcc aag ccc cgc ccc ccc tgg atg ggc ctg ctg 291  
  His Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu  
                   80                  85                  90

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  Gly Pro Thr Ile Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu  
                   95                  100                  105

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  Lys Asn Met Ala Ser His Pro Val Ser Leu His Ala Val Gly Val Ser  
                   110                  115                  120

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  Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln  
                   125                  130                  135

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  Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr  
                   140                  145                  150                  155



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tgc ctg acc tac agc tac ctg agc cac gtg gac ctg gtg aag gac ctg Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu 175 180 185	579
aac agc ggc ctg atc ggc gcc ctg ctg gtg tgc cgc gag ggc agc ctg Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu 190 195 200	627
gcc aag gag aag acc cag acc ctg cac aag ttc atc ctg ctg ttc gcc Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala 205 210 215	675
gtg ttc gac gag ggc aag agc tgg cac agc gag acc aag aac agc ctg Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu 220 225 230 235	723
atg cag gac cgc gac gcc gcc agc gcc cgc gcc tgg ccc aag atg cac Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His 240 245 250	771
acc gtg aac ggc tac gtg aac cgc agc ctg ccc ggc ctg atc ggc tgc Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys 255 260 265	819
cac cgc aag agc gtg tac tgg cac gtg atc ggc atg ggc acc acc ccc His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro 270 275 280	867
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cag acc ctg ctg atg gac ctg ggc cag ttc ctg ctg ttc tgc cac atc Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile 320 325 330	1011
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Glu	Asp	Thr	Leu	Thr	Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	
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Ser	Met	Glu	Asn	Pro	Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	
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Lys	Asn	Thr	Gly	Asp	Tyr	Tyr	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	
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Glu	Ile	Thr	Arg	Thr	Thr	Leu	Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr	
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gac	gac	acc	atc	agc	gtg	gag	atg	aag	aag	gag	gac	ttc	gac	atc	tac	2403
Asp	Asp	Thr	Ile	Ser	Val	Glu	Met	Lys	Lys	Glu	Asp	Phe	Asp	Ile	Tyr	
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Asp	Glu	Asp	Glu	Asn	Gln	Ser	Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	
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cac	tac	ttc	atc	gcc	gcc	gtg	gag	cgc	ctg	tgg	gac	tac	ggc	atg	agc	2499
His	Tyr	Phe	Ile	Ala	Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	
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Ser	Ser	Pro	His	Val	Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	

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Gln	Phe	Lys	Lys	Val	Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr			
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cag	ccc	ctg	tac	cgc	ggc	gag	ctg	aac	gag	cac	ctg	ggc	ctg	ctg	ggc	2643		
Gln	Pro	Leu	Tyr	Arg	Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly			
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Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala
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Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala
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cgc ctg cac ctg cag ggc cgc agc aac gcc tgg cgc ccc cag gtg aac      4035
Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn
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Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val
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acc ggc gtg acc acc cag ggc gtg aag agc ctg ctg acc agc atg tac      4131
Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr
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Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr
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ctg ttc ttc cag aac ggc aag gtg aag gtg ttc cag ggc aac cag gac      4227
Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp
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Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg
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Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
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Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile
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Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr
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Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	Val	Glu		
	770					775					780						
Met	Lys	Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn	Gln	Ser		
785					790					795					800		
Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala	Val		
				805					810					815			
Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	Leu	Arg		
			820					825					830				
Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	Val	Phe		
		835					840					845					
Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu		
	850					855						860					
Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val		
865					870					875					880		
Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr		
				885					890					895			
Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly		
			900					905					910				
Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr		
							920						925				
Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp		
	930					935					940						
Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val		
945					950					955					960		



His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	965	970	975
Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe	980	985	990
Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	Asn	Met	995	1000	1005
Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	Pro	Thr	1010	1015	1020
Phe	Lys	Glu	Asn	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp	1025	1030	1035
Thr	Leu	Lys	Gly	Leu	Val	Met	Ala	Gln	Asp	Gln	Arg	Ile	Arg	Trp	Tyr	1045	1050	1055
Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His	Phe	Ser	1060	1065	1070
Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met	Ala	Leu	1075	1080	1085
Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met	Leu	Pro	Ser	1090	1095	1100
Lys	Ala	Gly	Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly	Glu	His	Leu	His	1105	1110	1115
Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser	Asn	Lys	Cys	Gln	Thr	1125	1130	1135
Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile	Thr	Ala	1140	1145	1150
Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro	Lys	Leu	Ala	Arg	Leu	His	Tyr	1155	1160	1165
Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	Phe	Ser	Trp	Ile	1170	1175	1180
Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile	Lys	Thr	Gln	1185	1190	1195
Gly	Ala	Arg	Gln	Asn	Phe	Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	Ile	Ile	1205	1210	1215
Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn	Ser	1220	1225	1230
Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	1235	1240	1245
Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	1250	1255	1260
His	Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	1265	1270	1275
Gly	Cys	Asp	Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	1285	1290	1295
Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn	Met	1300	1305	1310
Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu	Gln	Gly	Arg	1315	1320	1325
Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys	Glu	Trp	Leu	Gln	1330	1335	1340
Val	Asp	Phe	Gln	Lys	Thr	Met	Lys	Val	Thr	Gly	Val	Thr	Thr	Gln	Gly	1345	1350	1355
Val	Lys	Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	Ser	1365	1370	1375
Ser	Ser	Gln	Asp	Gly	His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	Gly	Lys	1380	1385	1390
Val	Lys	Val	Phe	Gln	Gly	Asn	Gln	Asp	Ser	Phe	Thr	Pro	Val	Val	Asn	1395	1400	1405
Ser	Leu	Asp	Pro	Pro	Leu	Leu	Thr	Arg	Tyr	Leu	Arg	Ile	His	Pro	Gln			

1410	1415	1420
Ser Trp Val His Gln Ile Ala Leu Arg Met	Glu Val Leu Gly Cys Glu	
1425	1430	1435
Ala Gln Asp Leu Tyr		1440
1445		

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<220>  
 <223> synthetically generated peptide

<400> 4

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Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	Ala	Val	Glu	Leu	Ser
			20					25					30		
Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg
		35					40					45			
Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val
	50					55					60				
Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	His	Leu	Phe	Asn	Ile
65					70					75					80
Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln
				85					90					95	
Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser
			100					105					110		
His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser
		115						120				125			
Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp
	130					135					140				
Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu
145					150					155					160
Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser
				165					170					175	
Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile
		180						185					190		
Gly	Ala	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	
	195					200					205				
Gln	Thr	Leu	His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly
	210					215					220				
Lys	Ser	Trp	His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp
225					230					235					240
Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr
			245						250					255	
Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val
			260					265					270		
Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile
		275					280					285			
Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser
	290					295					300				
Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met
305					310					315					320
Asp	Leu	Gly	Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His
				325					330					335	

Asp	Gly	Met	Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro
			340					345					350		
Gln	Leu	Arg	Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp
		355					360					365			
Leu	Thr	Asp	Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser
	370					375					380				
Pro	Ser	Phe	Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	Gln	Gly	Lys	Thr
385					390					395					400
Trp	Val	His	Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro
				405					410					415	
Leu	Val	Leu	Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn
			420					425					430		
Asn	Gly	Pro	Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met
		435					440					445			
Ala	Tyr	Thr	Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu
	450					455					460				
Ser	Gly	Ile	Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu
465					470					475					480
Leu	Ile	Ile	Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro
				485					490					495	
His	Gly	Ile	Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys
			500					505					510		
Gly	Val	Lys	His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe
		515					520					525			
Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp
	530					535					540				
Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg
545					550					555					560
Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu
				565					570					575	
Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val
			580					585					590		
Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu
		595					600					605			
Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp
	610					615					620				
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625					630					635					640
Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp
				645					650					655	
Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe
			660					665					670		
Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr
	675						680					685			
Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro
	690					695					700				
Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly
705					710					715					720
Met	Thr	Ala	Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp
				725					730					735	
Tyr	Tyr	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys
			740					745					750		
Asn	Asn	Ala	Ile	Glu	Pro	Arg	Arg	Arg	Arg	Arg	Glu	Ile	Thr	Arg	Thr
		755					760					765			
Thr	Leu	Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser
	770					775					780				
Val	Glu	Met	Lys	Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn

785					790					795					800
Gln	Ser	Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala
				805					810					815	
Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val
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Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val
		835					840					845			
Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg
	850					855					860				
Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala
865					870					875					880
Glu	Val	Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg
				885					890					895	
Pro	Tyr	Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg
			900					905					910		
Gln	Gly	Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys
		915					920					925			
Thr	Tyr	Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu
	930					935					940				
Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys
945					950					955					960
Asp	Val	His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn
				965				970						975	
Thr	Leu	Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala
		980					985						990		
Leu	Phe	Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu
	995						1000					1005			
Asn	Met	Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp
	1010					1015				1020					
Pro	Thr	Phe	Lys	Glu	Asn	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile
1025					1030					1035					1040
Met	Asp	Thr	Leu	Pro	Gly	Leu	Val	Met	Ala	Gln	Asp	Gln	Arg	Ile	Arg
				1045					1050					1055	
Trp	Tyr	Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His
				1060				1065				1070			
Phe	Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met
		1075					1080				1085				
Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met	Leu
	1090					1095				1100					
Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly	Glu	His
1105					1110					1115					1120
Leu	His	Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser	Asn	Lys	Cys
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Gln	Thr	Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile
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Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro	Lys	Leu	Ala	Arg	Leu
		1155					1160					1165			
His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	Phe	Ser
	1170					1175					1180				
Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile	Lys
1185					1190					1195					1200
Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe
				1205					1210					1215	
Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly
			1220					1225					1230		
Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser
		1235					1240					1245			

Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile  
 1250 1255 1260  
 Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu  
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 Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu  
 1285 1290 1295  
 Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr  
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 Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln  
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 Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu Trp  
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 Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr  
 1345 1350 1355 1360  
 Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu  
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 Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn  
 1380 1385 1390  
 Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val  
 1395 1400 1405  
 Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His  
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<213> Artificial Sequence

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<223> Synthetic construct

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<400> 5

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16

<210> 6

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16

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 <213> Homo sapiens

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<210> 9  
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 <213> Homo sapiens

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 gggcctgctg ggccccctaca agctttac 88

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 <212> DNA  
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 tgcattgtag cctacgaatt ctac 84

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<213> Homo sapiens

<400> 13

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<210> 14

<211> 103

<212> DNA

<213> Homo sapiens

<400> 14

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caagggtgttc	cccggcgga	gccacaccta	cgtgtggcag	gtg		103

<210> 15

<211> 79

<212> DNA

<213> Homo sapiens

<400> 15

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<211> 107

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

<400> 17

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<211> 89

<212> DNA

<213> Homo sapiens

<400> 18

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<210> 19

<211> 122

<212> DNA

<213> Homo sapiens

<400> 19

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tc	122

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<210> 22  
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<400> 22	
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<210> 23  
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<400> 24	
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<400> 25	
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<210> 31  
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<212> DNA  
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<210> 33  
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<400> 34  
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<210> 35  
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 ccggcgaga tctctacaag ctttac 86

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<210> 38  
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 aagagcgacc cccgctgcct gaccgctac tacagcagct tc 102

<210> 42  
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<210> 43  
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 c 61

<210> 44  
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<400> 44

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gagaaccccg gcctgtggat ccctacaagc ttac 95

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ctgaagggga acagggtcag ggtgtcctcg tacaccatct tgtgcttgaa ggtgtagcc 119

<210> 51  
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 catg 124

<210> 52  
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<400> 52  
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 cgctggatgt tctcggtcag gtaccctacg aattctac 98

<210> 53  
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 ctggaggaga tcacccgcac caccctgcag agcgaccagg ag 102

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 gacgaggacg agaaccagag cccccgcagc ttccagaaga agacc 105

<210> 56  
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<400> 56  
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<210> 57

<211> 101  
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<210> 59  
 <211> 108  
 <212> DNA  
 <213> Homo sapiens

<400> 59  
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<400> 60  
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 cccaggatcc ctacgaattc tac 83

<210> 61  
 <211> 115  
 <212> DNA  
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<400> 61  
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<210> 62  
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 <212> DNA  
 <213> Homo sapiens

<400> 62  
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<400> 63  
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atccagatgg aggacccac cttcaaggag aactaccgct tccacg 106

<210> 64  
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<212> DNA  
<213> Homo sapiens

<400> 64  
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tccgctggta ccctacaagc ttac 85

<210> 65  
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<212> DNA  
<213> Homo sapiens

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gtgtccatga tgtagccgtt gatggcgtgg aagcggtagt tctccttgaa ggtgg 115

<210> 66  
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<212> DNA  
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accagctctt ggtctcgtcg aagatgggtga agaacaggg 99

<210> 67  
<211> 110  
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<400> 67  
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<210> 68  
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<400> 68  
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gcgcggttgc gcagcacgtg ctacgaattc tac 93

<210> 69  
<211> 116  
<212> DNA  
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<400> 69  
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<400> 70  
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<210> 71  
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 <213> Homo sapiens

<400> 71  
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 cacggccgcc aggtgaccct acaagcttta c 91

<210> 72  
 <211> 113  
 <212> DNA  
 <213> Homo sapiens

<400> 72  
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<210> 73  
 <211> 121  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
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<210> 74  
 <211> 93  
 <212> DNA  
 <213> Homo sapiens

<400> 74  
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<210> 75  
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<210> 76  
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<400> 76  
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 ag 122

<210> 77  
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 <212> DNA  
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<400> 77  
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<210> 78  
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 tactc 125

<210> 80  
 <211> 96  
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<210> 82  
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 <212> DNA  
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<210> 83  
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 caaccccccc gggctacaag ctttac 86

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 88

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&lt;210&gt; 89

&lt;211&gt; 89

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 89

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gaccatgaag	gtgaccctac	aagctttac				89

&lt;210&gt; 90

&lt;211&gt; 112

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

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&lt;210&gt; 91

&lt;211&gt; 114

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

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&lt;210&gt; 92

&lt;211&gt; 97

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 92

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&lt;210&gt; 93

&lt;211&gt; 122

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 93

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tc						122

&lt;210&gt; 94

&lt;211&gt; 104

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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 <213> Homo sapiens

<400> 96  
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<210> 97  
 <211> 100  
 <212> DNA  
 <213> Homo sapiens

<400> 97  
 cagggggggg tccaggctgt tcaccacggg ggtgaagctg tcctgggtgc cctggaacac 60  
 cttcaccttg ccgttctgga agaacagggt ccactgggtg 100

<210> 98  
 <211> 100  
 <212> DNA  
 <213> Homo sapiens

<400> 98  
 ccgtcctggc tgctgctgat caggaactcc ttcacgtaca tgctgggtcag caggctcttc 60  
 acgccctggg tggtcacgcc ggtcaccta cgaattctac 100

<210> 99  
 <211> 140  
 <212> DNA  
 <213> Homo sapiens

<400> 99  
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 tgctgaaggt gagcagctgc gacaagaaca ccggcgacta ctacgaggac agctacgagg 120  
 acatcagcgc ctacctgctg 140

<210> 100  
 <211> 57  
 <212> DNA  
 <213> Homo sapiens

<400> 100

agcaagaaca acgccatcga gccccgcagg cgcaggcgcg agatcacccg caccacc 57

<210> 101  
<211> 58  
<212> DNA  
<213> Homo sapiens

<400> 101  
ctgcagagcg accaggagga gatcgactac gacgacacca tcagcgtgga agctttac 58

<210> 102  
<211> 79  
<212> DNA  
<213> Homo sapiens

<400> 102  
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tggcgcgggt gatctcgcg 79

<210> 103  
<211> 57  
<212> DNA  
<213> Homo sapiens

<400> 103  
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<210> 104  
<211> 119  
<212> DNA  
<213> Homo sapiens

<400> 104  
ctcgtagctg tcctcgtagt agtcgccgggt gttcttgtcg cagctgctca ccttcagcag 60  
ggcggatcatg ccgcgggtgc ggaagtcgct gttgtggcag cccaggatcc gaattctac 119

<210> 105  
<211> 1505  
<212> DNA  
<213> Homo sapiens

<400> 105  
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aagatcctga accgccccaa gcgctacaac agcggcaagc tggaggagtt cgtgcagggc 180  
aacctggagc gcgagtgcac ggaggagaag tgcagcttcg aggaggcccc cgaggtgttc 240  
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agcaaccctt gcctgaacgg cggcagctgc aaggacgaca tcaacagcta cgagtgtctg 360  
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gatcc						1505

&lt;210&gt; 106

&lt;211&gt; 1352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

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tccccggcgc	ccgcgccctg	gacaacggcc	tggcccgcac	ccccaccatg	ggctggctgc	180
actgggagcg	cttcatgtgc	aacctggact	gccaggagga	gcccgcagagc	tgcattcagcg	240
agaagctgtt	catggagatg	gccgagctga	tggtagcgca	gggctggaag	gacgccggct	300
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ccagcttcaa	ccaggagcgc	atcgtggacg	tggccggccc	cgccggctgg	aacgaccccc	840
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tgtggggccat	catggccgcc	cccctgttca	tgagcaacga	cctgcgccac	atcagcccc	960
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agctgctgcc	cgtgaagcgc	aagctgggct	tctacgagtg	gaccagccgc	ctgcgcagcc	1260
acatcaaccc	caccggcacc	gtgctgctgc	agctggagaa	caccatgcag	atgagcctga	1320
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&lt;210&gt; 107

&lt;211&gt; 310

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetically generated construct

&lt;400&gt; 107

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gcgcttctgc	ttcagcgcca	cccgcgcgta	ctacctgggc	gccgtggagc	tgagctggga	120
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caagagcttc	cccttcaaca	ccagcgtggg	gtacaagaag	accctgttcg	tggagtccac	240
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caagctttac						310

<210> 108  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 108  
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 ccagcgaggg cgccgagtag gacgaccaga ccagccagcg cgagaaggag gacgacaagg 180  
 tgttccccgg cggcagccac acctacgtgt ggcaggtgct gaaggagaac ggcccatgg 240  
 ccagcgaccc cctgtgcctg acctacagct acctgagcca cgtgctacaa gcttttac 297

<210> 109  
 <211> 318  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 109  
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 tcctgctgtt cgccgtgttc gacgagggca agagctggca cagcgagacc aagaacagcc 180  
 tgatgcagga ccgcgacgcc gccagcgccc gcgcctggcc caagatgcac accgtgaacg 240  
 gctacgtgaa ccgcagcctg cccggcctga tcggctgcca ccgcaagagc gtgtactggc 300  
 acgtgctaca agcttttac 318

<210> 110  
 <211> 384  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 110  
 gtagaattcg tagcacgtga tcggcatggg caccaccccc gaggtgcaca gcatcttcct 60  
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 caccttcctg accgcccaga ccctgctgat ggacctgggc cagttcctgc tggtctgcca 180  
 catcagcagc caccagcacg acggcatgga ggctacgtg aaggtggaca gctgccccga 240  
 ggagccccag ctgcgcatga agaacaacga ggaggccgag gactacgacg acgacctgac 300  
 cgacagcgag atggacgtgg tgcgcttcga cgacgacaac agccccagct tcatccagat 360  
 ctctacggat cctacaagct ttac 384

<210> 111  
 <211> 443  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 111  
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 atcgccgccc aggaggagga ctgggactac gccccctgg tgctggcccc cgacgaccgc 120  
 agctacaaga gccagtacct gaacaacggc cccagcgca tcggccgcaa gtacaagaag 180  
 gtgcgcttca tggcctacac cgacgagacc ttcaagaccc gcgaggccat ccagcacgag 240  
 agcggcatcc tgggccccct gctgtacggc gaggtgggcg acaccctgct gatcatcttc 300  
 aagaaccagg ccagccgccc ctacaacatc tacccccacg gcatcaccga cgtgcgcccc 360  
 ctgtacagcc gccgctgccc caagggcggtg aagcacctga aggacttccc catcctgccc 420  
 ggcgagatct ctacaagctt tac 443

<210> 112

<211> 266

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 112  
 gtaaagcttg tagggtacca gctgcgggtc tcgtcgaaca cgctgaacag gatcacgttg 60  
 cgcttgctgc tcatgatctg gttgccgcgc tgggccacgc tctccttgta gcagatcagc 120  
 agggggccga tcaggccgct ggccaggctc cgctccatgt tcacgaagct gctgtagtag 180  
 cgggtcaggc agcgggggtc gctcttggtg gggccgtcct ccacggtcac ggtccacttg 240  
 tacttgaaga tctctacgaa ttctac 266

<210> 113

<211> 341

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 113  
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 gtgttcgaca gcctgcagct gagcgtgtgc ctgcacgagg tggcctactg gtacatcctg 180  
 agcatcggcg cccagaccga cttcctgagc gtgttcttca gcggtacac cttcaagcac 240  
 aagatgggtg acgaggacac cctgaccctg ttcccccttca gcggcgagac cgtgttcatg 300  
 agcatggaga accccggcct gtggatccct acaagcttta c 341

<210> 114

<211> 397

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 114  
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 gaggacatca ggcctacct gctgagcaag aacaacgcc a tcgagccccg cctggaggag 180  
 atcaccgcga ccaccctgca gagcgaccag gaggagatcg actacgacga caccatcagc 240  
 gtggagatga agaaggagga cttcgacatc tacgacgagg acgagaacca gagccccgc 300  
 agcttccaga agaagaccg ccactacttc atcgccgccc tggagcgcct gtgggactac 360  
 ggcagtagca gcagccccca cgtgctacaa gctttac 397



<210> 115  
 <211> 417  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 115  
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 gaaggtggtg ttccaggagt tcaccgacgg cagcttcacc cagcccctgt accgcggcga 120  
 gctgaacgag cacctggggc tgctggggcc ctacatccgc gccgaggtgg aggacaacat 180  
 catggtgacc gtgcaggagt tcgccctgtt cttcaccatc ttcgacgaga ccaagagctg 240  
 gtacttcacc gagaacatgg agcgcaactg ccgcgcccc tgcaacatcc agatggagga 300  
 cccaccttc aaggagaact accgcttcca cgccatcaac ggctacatca tggacaccct 360  
 gcccggcctg gtgatggccc aggaccagcg catccgctgg taccctacaa gctttac 417

<210> 116  
 <211> 327  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 116  
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 agcccaacga gaccaagacc tacttctgga aggtgcagca ccacatggcc cccaccaagg 180  
 acgagttcga ctgcaaggcc tgggcctact tcagcgacgt ggacctggag aaggacgtgc 240  
 acagcggcct gatcgcccc ctgctggtgt gccacaccaa caccctgaac cccgcccacg 300  
 gccgccaggt gaccctacaa gctttac 327

<210> 117  
 <211> 344  
 <212> DNA  
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<220>  
 <223> synthetically generated construct

<400> 117  
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 ctgtaccccg gcgtgttcga gaccgtggag atgctgcca gcaaggccgg catctggcgc 180  
 gtggagtgcc tgatcggcga gcacctgcac gccggcatga gcaccctgtt cctggtgtac 240  
 agcaacaagt gccagacccc cctgggcatg gccagcggcc acatccgca cttccagatc 300  
 accgccagcg gccagtacgg ccagtgggcc cctacaagct ttac 344

<210> 118  
 <211> 322  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 118  
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 cacggcatca agaccaggg cggccgccag aagttcagca gcctgtacat cagccagttc 180  
 atcatcatgt acagcctgga cggcaagaag tggcagacct accgcggcaa cagcaccggc 240  
 accctgatgg tggtcttcgg caacgtggac agcagcggca tcaagcaca catcttcaac 300  
 cccccgggc tacaagctt ac 322

<210> 119

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 119  
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 gggcatggag agcaaggcca tcagcgacgc ccagatcacc gccagcagct acttcaccaa 180  
 catgttcgcc acctggagcc ccagcaaggc ccgcctgcac ctgcagggcc gcagcaacgc 240  
 ctggcgcccc caggtgaaca accccaagga gtggctgcag gtggacttcc agaagaccat 300  
 gaaggtgacc ctacaagctt tac 323

<210> 120

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 120  
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 tccagaacgg caaggtgaag gtgttcagg gcaaccagga cagcttcacc cccgtggtga 180  
 acagcctgga cccccccctg ctgaccgcgt acctgcgcac ccacccccag agctgggtgc 240  
 accagatcgc cctgcgcacg gaggtgctgg gctgcgaggg ccaggacctg tactagctgc 300  
 ccgggctaca agctttac 318

<210> 121

<211> 310

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 121  
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 caggtggctg gtgaactcca cgaacagggt cttctgtac accacgctgg tggtgaagg 120  
 gaagctcttg ggcacgcggg gggggaagcg ggcgtccacg ggcagctcgc ccaggtcgc 180  
 ctgcatgtag tcccagctca gctccacggc gccaggtag tagcggcggg tggcgctgaa 240  
 gcagaagcgc agcaggcaca ggaagaagca ggtgctcagc tcgatctgca tgctagccta 300  
 cgaattctac 310

<210> 122  
 <211> 297  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 122  
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 tggggccgtt ctcccttcagc acctgccaca cgtaggtgtg gctgccgccg gggaacacct 120  
 tgtcgtcctc cttctcgcgc tggctgggtct ggtcgtcgtc ctccggcgccc tcgctggcct 180  
 tccagtagct cagcggccag gcgtgcaggc tcacgggggtg gctggccatg ttcttcaggg 240  
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<210> 123  
 <211> 318  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 123  
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 cgtcgcgggtc ctgcatcagg ctgttcttgg tctcgtgtg ccagctcttg cctcgtcga 180  
 acacggcgaa cagcaggatg aacttgtgca gggctctgggt cttctccttg gccaggctgc 240  
 cctcgcggga caccagcagg gcgccgatca ggccgctgtt caggctcctc accagggtcca 300  
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<210> 124  
 <211> 384  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 124  
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 cgcaccacgt ccatctcgt gtcggtcagg tcgtcgtcgt agtcctcggc ctccctcgtt 120  
 ttcttcatgc gcagctgggg ctccctcggg cagctgtcca ccttcacgta ggctccatg 180  
 ccgtcgtgct ggtggctgct gatgtggcag aacagcagga actggcccag gtccatcagc 240  
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 ccgatcacgt gctacgaatt ctac 384

<210> 125  
 <211> 443  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 125

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taggggcggc	tggcctgggt	cttgaagatg	atcagcaggg	tgtcgccac	ctcgccgtac	180
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ttcagggtact	ggctcttgta	gctgcgggtcg	tcggggggcca	gcaccagggg	ggcgtagtcc	360
cagtctctct	cctcggcggc	gatgtagtgc	accaggtct	tggggtgctt	cttggccacg	420
ctgcggatcc	ctacgaattc	tac				443

&lt;210&gt; 126

&lt;211&gt; 266

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetically generated construct

&lt;400&gt; 126

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aagagcgacc	cccgtgcct	gaccgctac	tacagcagct	tcgtgaacat	ggagcgcgac	120
ctggccagcg	gcctgatcgg	ccccctgctg	atctgctaca	aggagagcgt	ggaccagcgc	180
ggcaaccaga	tcattgagcga	caagcgcaac	gtgatcctgt	tcagcgtgtt	cgacgagaac	240
cgcagctggt	accctacaag	ctttac				266

&lt;210&gt; 127

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetically generated construct

&lt;400&gt; 127

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ctgaagaaca	cgctcaggaa	gtcgggtctgg	gcgccgatgc	tcaggatgta	ccagtagggc	180
acctcgtgca	ggcacacgct	cagctgcagg	ctgtcgaaca	cgtagccgtt	gatgctgtgc	240
atgatgttgc	tggcctggaa	ctcgggggtcc	tccagctgca	cgccggcggg	gttgggcagg	300
aagcgctgga	tgttctcggg	cagggtaccct	acgaattcta	c		341

&lt;210&gt; 128

&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetically generated construct

&lt;400&gt; 128

gtaaagcttg	tagcacgtgg	gggctgctgc	tcattgccgta	gtcccacagg	cgctccacgg	60
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cgctgtagat	gtcgaagtcc	tccttcttca	tctccacgct	gatggtgtcg	tcgtagtcga	180
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cggtgttctt	gtcgcagctg	ctcaccttca	gcagggcggt	catgccgcgg	ttgcggaagt	360
cgctgttgtg	gcagcccagg	atccctacga	attctac			397

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 <211> 417  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 129  
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 tccatctgga tgttgacagg ggcgcgagc ttgcgtcca tgttctcggg gaagtaccag 180  
 ctcttgggtc cgtcgaagat ggtgaagaac agggcgaact cctgcacggg caccatgatg 240  
 ttgtcctcca cctcggcgcg gatgtagggg ccagcaggc ccaggtgctc gttcagctcg 300  
 ccgcggtaca ggggctgggt gaagctgccg tcgggtgaact cctggaacac caccttcttg 360  
 aactggggca cgctgccgct ctgggcgcgg ttgcgcagca cgtgctacga attctac 417

<210> 130  
 <211> 327  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 130  
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 agggccaggc cttgcagtcg aactcgtcct tgggtgggggc catgtggtgc tgcaccttcc 180  
 agaagtaggt cttgggtctcg ttgggcttca cgaagtctt gcggggctcg gcgccctggc 240  
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 tgcggaaggt caccctacga attctac 327

<210> 131  
 <211> 344  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 131  
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 gtgctcatgc cggcgtgcag gtgctcgccg atcaggcact ccacgcgcca gatgccggcc 180  
 ttgctgggca gcatctccac ggtctcgaac acgccggggg acaggttgta cagggccatc 240  
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<210> 132  
 <211> 322  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

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<400> 132
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cgtccaggct gtacatgatg atgaactggc tgatgtacag gctgctgaac ttctggcgagg      180
cgccctgggt cttgatgccg tggatgatca tgggggccag cagggtccacc ttgatccagc      240
tgaagggttc cttggtgctc caggcgttga tgctgccgct gtagtgcagg cggggccagct      300
tgggggcccc tacgaattct ac                                          322

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<210> 133

<211> 323

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

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<400> 133
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tggggctcca ggtggcgaac atgttggtga agtagctgct ggcggtgatc tgggcgtcgc      180
tgatggcctt gctctccatg cccaggggca tgctgcagct gttcaggctc cagcccatca      240
gctccatgag cagggtgctg cggatgctgt agtgggtggg gtgcaggcgg atgtagcggg      300
cgatgatata ctacgaattc tac                                          323

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<210> 134

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

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<400> 134
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gggggggggc caggctgttc accacggggg tgaagctgct ctggttgccc tggaaacacct      180
tcaccttgcc gttctggaag aacagggtcc actggtggcc gtcctggctg ctgctgatca      240
ggaactcctt cacgtacatg ctggtcagca ggctcttcac gccctgggtg gtcacgcccg      300
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<210> 135

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

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<400> 135
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acatcagcgc ctacctgctg agcaagaaca acgccatcga gccccgcagg cgcaggcgcg      180
agatcacccg caccaccctg cagagcgacc aggaggagat cgactacgac gacaccatca      240
gcgtggaagc ttatc                                          255

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<210> 136

<211> 255

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetically generated construct

&lt;400&gt; 136

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tggtgcgggt	gatctcgcgc	ctgcgcctgc	ggggctcgat	ggcgttggtc	ttgctcagca	120
ggtaggcgct	gatgtcctcg	tagctgtcct	cgtagtagtc	gccggtgttc	ttgtcgcagc	180
tgctcacctt	cagcagggcg	gtcatgccgc	ggttgcggaa	gtcgtgtgtg	tggcagccca	240
ggatccgaat	tctac					255

&lt;210&gt; 137

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

Arg Arg Arg Arg

1

&lt;210&gt; 138

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

Arg Arg Arg Arg Arg

1

5

AI  
CONT.